Abstract

Method and system for predicting changes of physiological/pathological states in a patient, based on sampling, processing and analyzing a plurality of aggregated noisy biomedical signals. A reference database of raw data streams and/or features is generated by aggregating one or more raw data streams. The features are derived from the raw data streams and represent physiological/pathological states. Each feature consists of biomedical signals of a plurality of patients, wherein several patients have one or more of the physiological/pathological states. The features are obtained by performing, for each type of biomedical signal, adaptive segmentation of its corresponding raw data streams, and by assigning, to each segment, individual attributes that are represented by attribute values in order to obtain data related to each physiological/pathological states. Additional data streams using these attributes are generated and this process is repeated if needed. An attribute domain, in which each segment is represented by a point that corresponds to the attribute values of the segment is determined. A set of clusters is generated in the attribute domain for each physiological/pathological state. Each cluster consists of a combination of points determined by their relative location to other points, by assigning a set of property values to each point. Each property value corresponds to the degree of association of the point with one of the clusters, while associating each point, in time, to a corresponding state. The probabilities of transitions between states is determined by obtaining the frequency and the order of appearance of each point, in time. This process is repeated while in each time, the combination of points included in each cluster are varied according to their most updated property value and by including points derived from the probability until the updated property values remain essentially unchanged. By doing so, each cluster and the probabilities of transitions are updated. Prior knowledge data, consisting of a plurality of feasible paths between states according to the probabilities of transitions, is generated by associating each feasible path with a corresponding dynamics of transitions between physiological/pathological states. Updated clusters are associated with a normal/abnormal physiological state of the patient by using former knowledge, regarding normal/abnormal physiological/pathological states. For each patient, individual data streams and/or features, derived from the individual data streams are aggregated, while each individual data streams consists of biomedical signals of this patient. These features are obtained by performing, for each type of biomedical signal, adaptive segmentation of its corresponding raw data streams, and assigning, to each segment, individual attributes being represented by attribute values. Additional data streams are formed out of the attributes. Each individual attribute is assigned to a corresponding state, or to a new state, according to the probability to belong to each existing cluster or to a new cluster associated with the new or existing state and the probabilities of transitions. Each existing and/or new cluster and the probabilities of transitions are adaptively updated according to the individual data streams. A path, which is an individual dynamics, between physiological/pathological states is obtained according to their order of appearance. Then, a prediction of being in physiological/pathological states, or transitions to physiological/pathological states in the patient, is obtained by comparing the individual dynamics with known dynamics, obtained from prior knowledge.